

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/602,362

DATE: 07/07/2000

TIME: 17:10:54

Input Set : A:\LUD 5615.1 CIP Sequence listing ASCII Dos Text.txt

Output Set: N:\CRF3\07072000\I602362.raw

1 <110> APPLICANT: Jager, Dirk
 2 Scanlan, Matthew
 3 Gure, Ali
 4 Jager, Elke
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
 10 the Antigens per se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5615.1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/602,362
 C--> 16 <141> CURRENT FILING DATE: 2000-06-22
 18 <150> PRIOR APPLICATION NUMBER: 09/451,739
 20 <151> PRIOR FILING DATE: 1999-11-30
 E--> 22 <160> NUMBER OF SEQ ID NOS: 28

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

531 <210> SEQ ID NO: 16
 532 <211> LENGTH: 528
 533 <212> TYPE: PRT
 534 <213> ORGANISM: Homo sapiens
 535 <220> FEATURE:
 536 <400> SEQUENCE: 16

537 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 538 1 5 10 15
 540 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 541 20 25 30
 543 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 544 35 40 45
 546 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 547 50 55 60
 549 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 550 65 70 75 80
 552 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
 553 85 90 95
 555 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
 556 100 105 110
 558 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
 559 115 120 125
 561 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
 562 130 135 140
 564 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 565 145 150 155 160
 567 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
 568 165 170 175

512 (next page)
 global error - delete the numeric
 identifier if no
 C2217, C2227, or
 C2237 lines
 follow

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```

570 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
571      180      185      190
573 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
574      195      200      205
576 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
577      210      215      220
579 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
580 225      230      235      240
582 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 583      245      250      255
585 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 586      275      280      285
588 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 589      290      295      300
591 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu
E--> 592 305      310      315      320
594 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 595      325      330      335
597 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 598      340      345      350
600 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 601      355      360      365
603 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 604      370      375      380
606 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 607 385      390      395      400
609 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 610      405      410      415
612 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 613      420      425      430
615 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 616      435      440      445
618 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 619      450      455      460
621 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 622 465      470      475      480
624 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 625      485      490      495
627 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 628      500      505      510
630 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 631      515      520      525
716 <210> SEQ ID NO: 20
717 <211> LENGTH: 22
718 <212> TYPE: DNA
719 <213> ORGANISM: Homo sapiens
W--> 720 <220> FEATURE:
W--> 721 <400> SEQUENCE: 20
E--> 722 caagcagag cctcccgaga ag

```

← fix amino
acid nos.

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733 <210> SEQ ID NO: 22
 734 <211> LENGTH: (4095) 4115. (next page)
 735 <212> TYPE: DNA
 736 <213> ORGANISM: Homo sapiens
 W--> 737 <220> FEATURE:
 W--> 738 <400> SEQUENCE: 22

739	ctagtctata	cagcaacgac	cctacatcgt	cactctgggg	tcttagaaa	tcataaaagc	60
741	tgccctcccg	gacaagtcg	aagctggaga	gatgacaaa	ggaagaagac	atcaacctta	120
743	atatacaaga	gccagaga	gactgctcta	actgggctg	gtcaatggcc	tgaggaaagta	180
745	gtaacatttc	ggtagacaga	agtgccagct	gacgtccctg	tggcgaaacac	ggacacctct	240
747	gatgaaggct	tacaatgcc	caggaggctt	tgcaaatatt	tgatagattc	ggtgccgata	300
749	taaatctcgt	gatgtgtatg	caacatggct	tccattatgc	gtttatagtg	gattttgtca	360
751	gtggtggcaa	actgctgtcc	atggtgcagt	atcgaaagtc	caacaaggct	gcctcacacc	420
753	acttttacta	ccataacgaa	agaagtgagc	aattgtgaa	ttttgctgat	aaaaatgcaa	480
E--> 754							540
E--> 755	atgcgaatgc	gttaataagt	taaatgcaca	ccctcatgct	gctgtatgtc	tggatcatca	600
E--> 756							660
E--> 757	gagatagttg	catgcttctt	agcaaaatgt	gacgtctttg	tgcatatata	gtggagtaac	720
E--> 758							780
E--> 759	tgcaagaacat	atgctgttac	tgtgggatttc	tcacattcat	aacaaattat	gaatatatac	840
E--> 760							900
E--> 761	gaaaattatc	aaaaatcatc	aaataccaat	cagaaggaac	tctgcaggaa	acctgatgag	960
E--> 762							1020
E--> 763	gctgcaccct	ggcggaagaa	cacctgacac	gctgaaagct	ggtggaaaaa	cacctgatga	1080
E--> 764							1140
E--> 765	ggctgcacc	tggtggaaag	acacctgaca	ggctgaaagc	tggtggaaaa	acacctgatg	1200
E--> 766							1260
E--> 767	aggtgcac	ttgtggagg	aacatctgac	aaattcaatg	ttggagaaag	gacatctgga	1320
769	aagttcgaac	gtcagcagaa	aaacccctag	gaaattacga	tcctgcaaaa	aaacatctga	1380
771	gaaatttacg	ggccagcaaa	ggaagaccta	gaagatcgca	gggagaaaaa	gaagacacac	1440
773	ctagggaat	atgagtcgcc	aaaagaaaca	ctgagaaatt	acgtgggcag	aaaaggaaga	1500
775	cctaggaaga	cgcatgggag	aaaaagaaac	cctgtaaaga	tggatgcgtg	caagagtaac	1560
777	atctaataaa	ctaaagtgtt	gaaaaaggaa	atctaagatg	ttgcatgtcc	acaaaagaat	1620
779	catctacaaa	gcaagtgcca	tgatcagagg	tccatcaga	tccaaacaag	ggaagatgaa	1680
781	gaatattctt	tgattctcgg	gtctctttga	agttctgcaa	gattcaagtg	gtataacctga	1740
783	gtctatatat	aaaaagtaat	gagataaata	agaagtagaa	agcctcctaa	aagccatctg	1800
785	ccttcaagcc	gccattgaaa	gcaaaactct	ttccaaataa	gcctttgaat	gaagaatgaa	1860
787	caaacattga	agcagatccg	tgttcccacc	gaatccaaac	aaaggactat	aagaaaattc	1920
789	ttgggattct	agagtctctg	gagactgttt	acagaaggat	tgtgtttacc	aaggctacac	1980
791	atcaaaaaga	atagataaaa	aaatggaaaa	tagaagagtc	cctaataaag	tggtcttctg	2040
793	aaggctacct	cggaatgaaa	tttctattcc	actaaagcct	agaattgaag	acatgcaaac	2100
795	tttcaaaagc	agcctccggg	aagccatctg	cttcgagcct	ccactgaaat	caaaagtctg	2160
797	ttccaaataa	gccttggaat	gaaaaatgaa	aaacatggag	gcagatgaga	actcccatca	
799	gaatccaaac	aaaggactat	aagaaaattc	tgggatactg	gagtctctgt	agactgtttc	
801	acagaaggat	tgtgtttacc	aaggctgcgc	tcaaaaagaa	tagataaaat	aatggaaaaa	
803	tagaagggtc	cctgtttaaag	tggcttctctg	aggctaactg	ggaatgaaag	ttctattcca	
805	actaaagcct	agaattgatg	acatgcaaac	ttcaaaagcag	gcctcccgag	agccatctgc	
807	cttcgagcct	ccattgaaat	caaaagtctg	ttcaaaataa	ccttggaatt	aagaatgaac	
809	aaacattgag	gcagatgaga	actcccatca	aatccaaaca	aaggactatg	agaaagtctt	

move down

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```

811 tgggattctg gagtctctgt agactgtttc cagaaggatg gtgtttaccc aggctacaca 2220
813 tcaaaaagaa tagataaaat aatggaaaaa agaagagtct ctgataatga ggttttctga 2280
815 aggtccctcg agaatagaag ttctattcca ctaaagcctt gaattgatgg catgcaaaact 2340
817 ttcaaaagcag gcctcccagag agccatctgc ttcgagcctg cattgaaatg aaaagtctgt 2400
819 tcaaaaataa ccttggaatt aagaatgaac aacattgaga cagatcagat ttcccttcag 2460
821 aatcaaaaaca aagaagggtg agaaaattct gggattctga agtctccgtg gactgtttca 2520
823 cagaaggatg gtgtgtaccc aggctacaca caaaaagaaa ggataaaata gtggaaaatt 2580
825 agaagattca ctagcctatc aaaatcttgg tacagttcat cttgtgaaag gcaagggaaac 2640
827 ttcaaaaaga cactgtgaac acgtacagga aaatggaaca atgaaaaaga gttttgtgta 2700
829 ctgaaaaaga actgtcagaa caaaaagaaat aaatcacagt agagaaccaa aagttaaattg 2760
831 ggaacaagag tctgcagtgt agattgaact aaaccaagaa aagagaagag agaaatgccg 2820
833 atatattaaa gaaaaaatta ggaagaatta gaagaatcga gacgagcata gaaagagtta 2880
835 gaagtgaac acaacttgaa aggcctctcag atacaagata agaattgaag gtgtagaaag 2940
837 taatttgaat aggttttcca actcatgaaa tgaataattat tcttacctga aattgcatgt 3000
839 tgaaaaagga attgccatgc aaaactggaa tagccacact aaacaccaat ccaggaaaag 3060
841 gaaaataaat ctttgaggac ttaagatttt aaagaaaaga tgctgaactt agatgaccct 3120
843 aaaactgaaa aggaatcatt actaaaaggg atctcaatat gtgggcagct aaagtcttga 3180
845 tagctgagaa acaatgctca ttctaaattg aggaaaaaca gacaaagaaa actagaggca 3240
847 gaaattgaat acaccatcct gactggcttc gctgtacaag ccatgatcaa ttgtgacatc 3300
849 aagaaaaagt aagaacctgc ttccacattg aggagatgct gtttgcaag aaaaatgaatg 3360
851 ttgatgtgag agtacgatat taacaatgag tgctccatca ccactttctg agctcaaagg 3420
853 aaatccaaaa cctaaaaatt atctcaatta gcaggagatg tctaagagaa atacattggt 3480
855 ttcagaacat cacaagaga caacgtgaaa acagtgtcaa tgaaggaaagc gaacacatgt 3540
857 atcaaaacga caagataatg gaacaaacac ctgaacagca gagtctctag tcagaaaatta 3600
859 ttccaactac aagcaaaaat tgtggcttca cagcaattag tcatgcacat agaagctga 3660
E--> 861 caaaaaagc agataacaat gatattcatt tcttgagagg aatgcaaca catctcctaa 3720
E--> 863 aagagaaaaa gaggagatat taattacaat accatttaa aaccgtatat tcaatatgaa 3780
E--> 865 aaagagaaag agaacagaa actcatygaa acaagcagta gaaacttctt tggagaaaca 3820
E--> 867 acagaccaga ctttactcac actcatgcta gaggccagtc tagcatcacc tatgttgaaa 3880
E--> 869 atcttaccaa agtctgtgtc acagaatact attttagaag aaaattcatg tttcttctg 3940
E--> 871 aagcctacag cataaaataa agtgtgaaga ttacttgctt cgaattgcat aagctgcaca 4000
E--> 873 ggattcccat taccctgatg tgcagcagac tcattcaatc aaccagaatc cgctctgcac 4060
E--> 875 tccagcctag tgacagagtg gactccactt ggaaa 4095
E--> 1136 <210> SEQ ID NO: 23 24 ← should be - seq 23 already in file
1137 <211> LENGTH: 24
1138 <212> TYPE: DNA
1139 <213> ORGANISM: Homo sapiens
W--> 1140 <220> FEATURE
W--> 1141 <400> SEQUENCE: 23 24
E--> 1142 aatgggaa 41 agagctctgc ag 22
E--> 1144 <210> SEQ ID NO: 25

```

discrepancy

"4" is not a nucleotide

3720 3780

↓ numbers off

pyl

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\LUD 5615.1 CIP Sequence listing ASCII Dos Text.txt
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L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:39 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:90 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:283 W: Missing Blank Line separator, <220> field identifier
L:138 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:283 W: Missing Blank Line separator, <220> field identifier
L:171 M:283 W: Missing Blank Line separator, <400> field identifier
L:207 M:283 W: Missing Blank Line separator, <220> field identifier
L:208 M:283 W: Missing Blank Line separator, <400> field identifier
L:268 M:283 W: Missing Blank Line separator, <220> field identifier
L:269 M:283 W: Missing Blank Line separator, <400> field identifier
L:317 M:283 W: Missing Blank Line separator, <220> field identifier
L:318 M:283 W: Missing Blank Line separator, <400> field identifier
L:369 M:283 W: Missing Blank Line separator, <220> field identifier
L:372 M:283 W: Missing Blank Line separator, <400> field identifier
L:395 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:395 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:404 M:283 W: Missing Blank Line separator, <220> field identifier
L:405 M:283 W: Missing Blank Line separator, <400> field identifier
L:413 M:283 W: Missing Blank Line separator, <220> field identifier
L:414 M:283 W: Missing Blank Line separator, <400> field identifier
L:422 M:283 W: Missing Blank Line separator, <220> field identifier
L:423 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <220> field identifier
L:432 M:283 W: Missing Blank Line separator, <400> field identifier
L:440 M:283 W: Missing Blank Line separator, <220> field identifier
L:441 M:283 W: Missing Blank Line separator, <400> field identifier
L:449 M:283 W: Missing Blank Line separator, <220> field identifier
L:450 M:283 W: Missing Blank Line separator, <400> field identifier
L:458 M:283 W: Missing Blank Line separator, <220> field identifier
L:461 M:283 W: Missing Blank Line separator, <400> field identifier
L:516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:516 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:524 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:526 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:528 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:535 M:283 W: Missing Blank Line separator, <220> field identifier
L:536 M:283 W: Missing Blank Line separator, <400> field identifier
L:583 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:631 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:512 SEQ:16

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L:638 M:283 W: Missing Blank Line separator, <220> field identifier
L:639 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:283 W: Missing Blank Line separator, <220> field identifier
L:648 M:283 W: Missing Blank Line separator, <400> field identifier
L:656 M:283 W: Missing Blank Line separator, <220> field identifier
L:657 M:283 W: Missing Blank Line separator, <400> field identifier
L:720 M:283 W: Missing Blank Line separator, <220> field identifier
L:721 M:283 W: Missing Blank Line separator, <400> field identifier
L:722 M:254 E: No. of Bases conflict, LENGTH:Input:22 Counted:21 SEQ:20 ✓
L:722 M:252 E: No. of Seq. differs, <211>LENGTH:Input:22 Found:21 SEQ:20 ✓
L:728 M:283 W: Missing Blank Line separator, <220> field identifier
L:729 M:283 W: Missing Blank Line separator, <400> field identifier
L:737 M:283 W: Missing Blank Line separator, <220> field identifier
L:738 M:283 W: Missing Blank Line separator, <400> field identifier
L:754 M:254 E: No. of Bases conflict, LENGTH:Input:540 Counted:480 SEQ:22 ✓
M:254 Repeated in SeqNo=22
L:875 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4095 Found:4115 SEQ:22 ✓
L:881 M:283 W: Missing Blank Line separator, <220> field identifier
L:882 M:283 W: Missing Blank Line separator, <400> field identifier
L:1136 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:23 ✓
L:1140 M:283 W: Missing Blank Line separator, <220> field identifier
L:1141 M:283 W: Missing Blank Line separator, <400> field identifier
L:1142 M:254 E: No. of Bases conflict, LENGTH:Input:22 Counted:21 SEQ:23 ✓
L:1142 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓
L:1142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:21 SEQ:23 ✓
L:1144 M:214 E: (33) Seq.# missing, SEQ ID NO:24 ✓
L:1148 M:283 W: Missing Blank Line separator, <220> field identifier
L:1149 M:283 W: Missing Blank Line separator, <400> field identifier
L:1175 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1175 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1219 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
M:340 Repeated in SeqNo=26
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (28) Counted (29) ✓